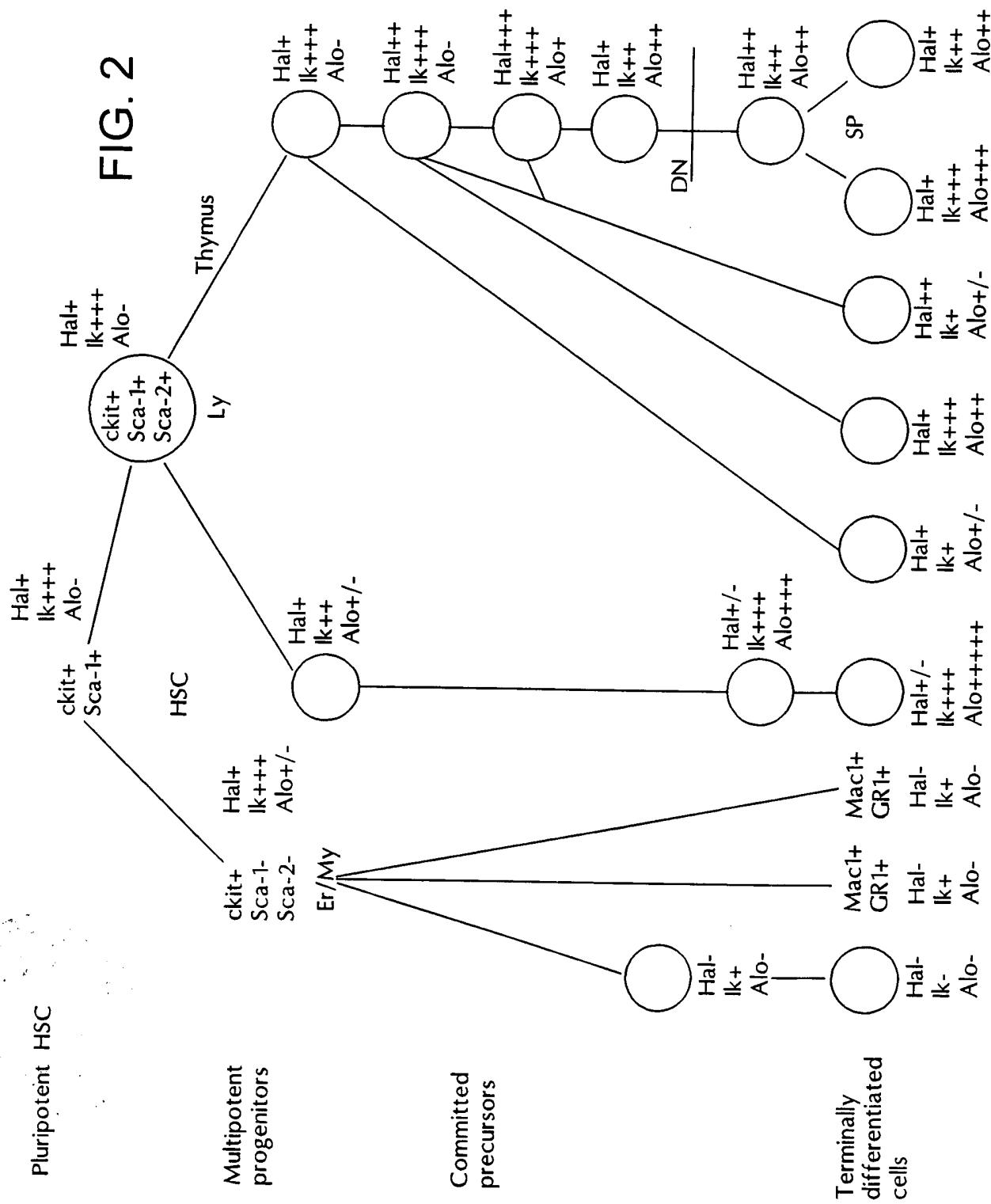


FIG.

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FIG. 2



ATG GAAACAGACGGCTATTGATGGCTATATAACATGTGACAATGAGCTTCACCCGAAGGGAAACACGCCA
TAC CTTTGTCTGCGATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGGCTTCCCCTTGCGGGT 70
M E T D A I D G Y I T C D N E L S P E G E H A
ATA TG GCC ATT GAC CT CAC CT CA AGC AC G C C C A AT GG AC AG C AC G C C T C G C C A A G T C A C AT G A C A A G C A C
TAT ACC CG GT A ACT GG AG T GG AG T TC G T G C G G G T T A C C T G T C G T G C G G A G C G G T C A G T G T A C T G T T C G T G 140
N M A I D L T S S T P N G Q H A S P S H M T S T
AAA TT CT GT AA AG C T G G A A T G C A G A G T G A A G A G T G T G A C A G G C A G C C C T G A G C C G T G A G G A T G A G
TTT A A G A C A T T C G A C C T T A C G T C T C A C T T C T C A C A C T G T C C G T C G G G A C T C G G C A C T C C T A C T C 210
N S V K L E M Q S D E E C D R Q P L S R E D E
ATC A G G G G C C A C G A T G A G G G G A G C A G C C T A G A A G A A C C C C T A A T T G A G A G C A G C G A G G T G G C C G A C A A C A
TAG T C C C C G G T G C T A C T C C C C T C G T C G G A T C T T C T T G G G G A T T A A C T C T C G T C G C T C C A C C G G C T G T T G T 280
I R G H D E G S S L E E P L I E S S E V A D N
G G A A A G T C C A G G A C C T C A A G G C G A G G G A G G A A T C C G G C T C C G A A T G G T A A A C T G A A A T G T G A C G T C T G
C C T T T C A G G T C C T G G A A G T C C G C T C C C T C C T T A G G C C G A A G G C T T A C C A T T G A C T T A C T G C A G A C 350
R K V Q D L Q G E G G I R L P N G K L K C D V C
T G G C A T G G T T G C A T T G G G C C A A T G T G C T T A T G G T A C A T A A A A G G A G T C A C A C T G G T G A G C G G C C C T C
A C C G T A C C A A A C G T A A C C C G G G T T A C A C G A A T A C C A T G T A T T T C C T C A G T G T G A C C A C T C G C C G G G A A G 420
G M V C I G P N V L M V H K R S H T G E R P F
C A C T G T A A C C A G T G C G G A G C T T C T T T A C C C A G A A G G G C A A C T T C T G A G A C A G A T A A A G T T A C A C T C G
G T G A C A T T G G T C A C G C C T C G A A G A A A A T G G G T C T T C C C G T T G G A A G A C T C T G T G T A T T C A A T G T G A G A C 490
H C N Q C G A S F T Q K G N L L R H I K L H S
G A G A G A A G C C C T T C A A A T G T C C T T C T G T A G C T A T G C T T G T A G A A G A A G G G A C C G C T C A C A G G A C A C C T
C T C T C T T C G G G A A G T T T A C A G G A A A G A C A T C G A T A C G A A C A T C T T C T C C C T G C G A G A G T G T C C T G T G G A 560
G E K P F K C P F C S Y A C R R R D A L T G H L
C A G G A C C C A T T C T G T G G G T A A A C C T C A C A A G T G T A A C T A C T G T G G C C G A A G G C T A C A A G C A G C G C A C G T C A
G T C C T G G G T A A G A C A C C C A T T G G A G T G T T C A C A T T G A T G A C A C C G G C T T C G A T G T T C G T C G C G T G C A G T 630
R T H S V G K P H K C N Y C G R S Y K Q R T S

FIG. 3A

CTGGAGGAACACAAGGAACCGCTGTCAACAATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCA
GACCTCCTTGTGTTCTTGCACAGTGTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCCTCCAGT 700
L E E H K E R C H N Y L Q N V S M E A A G Q V
TGAGTCACCATGTAACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATCATGGACAACAATATTCCTCT
ACTCAGTGGTACATGGCGGATACTTCTAACATTCCTGTTCTGGATAGTACCTGTTATAAAGAGA 770
M S H H V P P M E D C K E Q E P I M D N N I S L
GGTGCCTTTGAGAGACCTGCTGTCAAGAGAAGCTCACGGCAAATATGGAAAGCGAAAAGCTCCACT
CCACGGAAAACCTCTGGACGACAGTATCTCTCGAGTGCCTGTTATACCTTCGCGTTTCGAGGTGA 840
V P F E R P A V I E K L T A N M G K R K S S T
CCTCAGAAGTTGTGGGGAAAAGCTTATGCGATTCACTACCCAGATATTCACTTTGATATGAACCTAA
GGAGTCTTCAAACACCCCCCTTTCGAATACGCTAACGCTAGTCGATGGGTCTATAAGTAAACTATACTTGAATT 910
P O K F V G E K L M R F S Y P D I H F D M N L
CATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTA
GTATACTCTTCCGACTCGACTACGTCAGAGTATACTACCTGGTTGGTAGTTGTTACGTTAGTGGAT 980
T Y E K E A E L M Q S H M M D Q A I N N A I T Y
CCTTGGAGCTGAGGCCCTCACCTCTGATGCAGCATGCACCAAGCACAAATCGCTGAGGTGGCCCCAGTT
GGAACCTCGACTCCGGAAAGTGGAGACTACGTCGTACGTGGTTGTAGCGACTCCACCGGGTCAA 1050
L G A E A L H P L M Q H A P S T I A E V A P V
ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTG
TATTCGAGTCGAATAAGAGTCAGATAGTAGGTTGTCTATCTTCTGGTAATCGTCCCTTGAGAC 1120
I S S A Y S Q V Y H P N R I E R P I S R E T S
ATAGTCACGAAACACATGGATGGCCCCATCTCTCATCAGACCAAAGAGTCGACCCAGGAAAGAGA
TATCAGTGCTTGTGTTACCTACCGGGTAGAGAGAGTAGTCTGGTTCTCAGCTGGGTCTTCTCT 1190
D S H E N N M D G P I S L I R P K S R P Q E R E
GGCCTCGCCCAGCAATAGCTGCCCTGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCTAC
CCGGAGCGGGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTCTCGGTACTACTGGCGGTCAAGGATG 1260
A S P S N S C L D S T D S E S S H D D R Q S Y

FIG. 3B

CAAGGAAACCTGCCTTAAATCCAAAGAGGAAACAAAGCCCAGCTTACATGAAGGAGGATGTCAAGGCTT 1330
GTTCTTGGGACGGAATTAGGTTCTCCTTGTTGGGTCGAATGTACTTCCTCCTACAGTTCCGAA
Q G N P A L N P K R K Q S P A Y M K E D V K A
TGGATGCTACCAAGGCCCCAAGGGCTCTCTGAAGGACATCTATAAGGTTTCAATGGAGAAGGAGAAC 1400
ACCTACGATGGTTCCGGGGTCCCGAGAGACTTCCTGTAGATATTCCAAAAGTTACCTCTTCCCTTTGT
L D A T K A P K G S L K D I Y K V F N G E G E Q
GATAAGGGCTTCAAGTGTGAGCACTGCCGAGTCCTTTCTAGACCATGTACATGTACACCATTACATG 1470
CTATTECCCGAAGTTCACACTCGTGACGGCTCAGGAAAAGATCTGGTACAGTACATGTGGTAAGTGTAC
I R A F K C E H C R V L F L D H V M Y T I H M
GGTTGCCATGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAAT 1540
CCAACGGTACCGATGGCCCTGGGTGACCTACGTTAGACACCGATGTCTCGGTCTGGCGATGCTTA
G C H G Y R D P L E C N I C G Y R S Q D R Y E
TTTCATCACACATTGTTGGGGGCAGCACACATTCCACTAGGCCTTGCAATTCCAAGG 1598
AAAGTAGTGTGTAACAACCCCCCGTCGTGTAAAGGTGATCCGCAAACGTAAGGTTCC
F S S H I V G G Q H T F H A F A F Q G

FIG. 3C

ATGGAAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTCACCCGAAGGGAAACACGCCA
TACCTTTGTCTGCATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGCTTCCCCTTGCGGT 70
M E T D A I D G Y I T C D N E L S P E G E H A
ATATGGCCATTGACCTCACCTCAAGCACGCCAATGGACAGCACGCCCTGCCAAGTCACATGACAAGCAC
TATAACCGGTAACTGGAGTGGAGTTCGTGCGGGTTACCTGTCGTGCGGAGCGGTTCA GTGTACTGTTCGTG 140
N M A I D L T S S T P N G Q H A S P S H M T S T
AAATTCTGTAAAGCTGGAAATGCAGAGTGATGAAGAGTGACAGGCAGCCCTGAGCCGTGAGGATGAG 210
TTAACAGACATTCGACCTTACGTCTCACTTCTCACACTGTCCGTGGGACTCGGCACTCCTACTC
N S V K L E M Q S D E E C D R Q P L S R E D E
ATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCCTAATTGAGAGCAGCGAGGTGGCCGACAACA
TAGTCCCCGGTGTACTCCCTCGTCGGATCTTCTGGGATTAACTCTCGTCGTCCACCGGCTGTTGT 280
I R G H D E G S S L E E P L I E S S E V A D N
GGAAAGTCCAGGACCTTCAAGGCAGGGAGGAATCCGGCTCCGAATGGTGAGCGGCCCTCCACTGTAA
CCTTCAGGTCTGGAAAGTTCGCTCCCTCCTAGGCCAAGGCTTACCACTGCCGGAAAGGTGACATT 350
R K V Q D L Q G E G G I R L P N G E R P F H C N
CCAGTGCAGGAGCTTCTTACCCAGAAGGGCAACCTCTGAGACACATAAAGTTACACTCTGGAGAGAAG
GGTCACCCCTCGAAGAAAATGGGTCTCCGTTGGAAAGACTCTGTGTATTCAATGTGAGACCTCTCTTC 420
Q C G A S F T Q K G N L L R H I K L H S G E K
CCCTTCAAATGTCTTCTGTAGCTATGCTGTAGAAGAAGGGACGCCCTCACAGGACACCTCAGGACCC
GGGAAGTTACAGGAAAGACATCGATAACATCTTCTCCCTGCAGAGTGTCTGTGGAGTCCCTGGG 490
P F K C P F C S Y A C R R R D A L T G H L R T
ATTCTGTGGTAAACCTCACAGTGTAACTACTGTGGCCGAAGCTACAAGCAGCGCACGTCACTGGAGGA
TAAGACACCCATTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCGTCGCGTGCAGTGACCTCCT 560
H S V G K P H K C N Y C G R S Y K Q R T S L E E
ACACAAGGAACGCTGTACAAACTATCTCAGAATGTCAGCATGGAGGCTGCCGGCAGGTATGAGTCAC
TGTGTTCTTGCAGTGTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGTACTCAGTG 630
H K E R C H N Y L Q N V S M E A A G Q V M S H

FIG. 4A

CATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATCATGGACAACAATATTCTCTGGTGCCTT
700
GTACATGGCGGATACCTCTAACATTCTGTTCTGGATAGTACCTGTTATAAAGAGACCAACGGAA
H V P P M E D C K E Q E P I M D N N I S L V P
TTGAGAGACCTGCTGTATAGAGAACGTCACGGCAAATATGGGAAAGCGCAAAAGCTCCACTCCTCAGAA
770
AACTCTCTGGACGACAGTATCTCTTGAGTGCCGTTTATACCCCTTCGCGTTTCGAGGTGAGGAGTCTT
F E R P A V I E K L T A N M G K R K S S T P Q K
GTTTGTGGGGAAAAGCTTATGCATTAGCTACCCAGATATTCACTTGATATGAACCTAACATATGAG
840
CAAACACCCCCCTTTCGAATACGCTAAGTCGATGGTCTATAAGTAAACTATACTTGAATTGTATACTC
F V G E K L M R F S Y P D I H F D M N L T Y E
AAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTACCTTGGAG
910
TTCCCTCCGACTCGACTACGTCAAGAGTATACTACCTGGTTCGGTAGTTACGTTAGTGGATGGAACCTC
K E A E L M Q S H M M D Q A I N N A I T Y L G
CTGAGGCCCTTCAACCTCTGATGCAGCATGCCACCAAGCACAATCGCTGAGGTGGCCCCAGTTATAAGCTC
980
GACTCCGGGAAGTGGGAGACTACGTCTACGTGGTTCTGTTAGCGACTCCACCGGGTCAATATTGAG
A E A L H P L M Q H A P S T I A E V A P V I S S
AGCTTATTCTCAGGTCTATCATCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTGATAGTCAC
1050
TCGAATAAGAGTCCAGATAGTAGGTTGCTATCTTCTGGTAATCGTCCCTTGTAGACTATCAGTG
A Y S Q V Y H P N R I E R P I S R E T S D S H
GAAAACAACATGGATGGCCCCATCTCTCATCAGACCAAGAGTCGACCCAGGAAAGAGAGGCCCTCGC
1120
CTTTTGTGTACCTACCGGGTAGAGAGAGTAGTCTGGTTCTCAGCTGGGTCTTCTCCGGAGCG
E N N M D G P I S L I R P K S R P Q E R E A S
CCAGCAATAGCTGCCCTGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCTACCAAGGAAA
1190
GGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTCATCGTACTACTGGCGGTCAAGGATGGTTCTT
P S N S C L D S T D S E S S H D D R Q S Y Q G N
CCCTGCCCTAAATCCCAAGAGGAAACAAAGCCAGTACATGAAGGAGGATGTCAGGCTTGGATGCT
1260
GGGACGGAATTAGGGTTCTCCTTGTTCGGTCGAATGTACTCCTACAGTCCGAAACCTACGA
P A L N P K R K Q S P A Y M K E D V K A L D A

FIG. 4B

ACCAAGGGCCCCAAGGGCTCTGAAGGACATCTATAAGGTTCAATGGAGAACAGATAAGGG
TGGTTCCGGGGGTTCGGAGAGACTTCCTGTAGATATTCCAAAAGTTACCTCTCCTCTTGTCTATTCCC 1330
T K A P K G S L K D I Y K V F N G E G E Q I R
CCTTCAAGTGTGAGCACTGCCGAGTCCTTTCTAGACCATGTCATGTACACCATTACATGGGTTGCCA
GGAAGTTCACACTCGTGACGGCTCAGGAAAAAGATCTGGTACAGTACATGTGGTAAGTGTACCCAACGGT 1400
A F K C E H C R V L F L D H V M Y T I H M G C H
TGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAACGCCAGGACCGCTACGAATTTCATCA
ACCGATGGCCCTGGGTGACCTTACGTTAGACACCGATGTCTCGGTCTGGCGATGCTAAAGTAGT 1470
G Y R D P L E C N I C G Y R S Q D R Y E F S S
CACATTGTTGGGGGCAGCACACATTCCACTAGGC GTTGCATTCCAAGG
GTGTAACAACCCCCCGTCGTGTAGGTGATCCGCAAACGTAAGGTTCC 1520
H I V G G Q H T F H A F A F Q G

FIG. 4C

1/1 31/11
GCC CGG GCA GGT CGC ATT GCT ATA GCA CTG ACT GAC CTC TCT CTC TCT CTT TTT TTT CCT
A R A G R I A I A L T D L S L S L F F P
61/21 91/31
CTT TCC TGA AAC CCG ACA TTG TCA CCT CCT CTT TGA GGG TTA GAA GAA GCT GAG ATC TCC
L S * N P T L S P P L * G L E E A E I S
121/41 151/51
CGA CAG AGC TGG AAA TGG TGA TGA ATC TTT TTT AAT CAA AGG ACA ATT TCT TTT CAT TGC
R Q S W K W * * I F F N Q R T I S F H C
181/61 211/71
ACT TTG ACT ATG GAA ACA GAG GCT ATT GAT GGC TAT ATA ACG TGT GAC AAT GAG CTT TCA
T L T M E T E A I D G Y I T C D N E L S
241/81 271/91
CCC GAA AGG GAG CAC TCC AAT ATG GCA ATT GAC CTC ACC TCA AGC ACA CCC AAT GGA CAG
P E R E H S N M A I D L T S S T P N G Q
301/101 331/111
CAT GCC TCA CCA AGT CAC ATG ACA AGC ACA GAT TCA GTA AAG CTA GAA ATG CAG AGT GAT
H A S P S H M T S T D S V K L E M Q S D
361/121 391/131
GAA GAG TGT GAC AGG AAA CCC CTG AGC CGT GAA GAT GAG ATC AGG GGC CAT GAT GAG GGT
E E C D R K P L S R E D E I R G H D E G
421/141 451/151
AGC AGC CTA GAA GAA CCC CTA ATT GAG AGC AGC GAG GTG GCT GAC AAC AGG GAA GTC CAG
S S L E E P L I E S S E V A D N R E V Q
481/161 511/171
GAG CTT CAA GGC GAG GGA GGA ATC CGG CTT CCG AAT GGT AAA CTG AAA TGT GAC GTC TGT
E L Q G E G G I R L P N G K L K C D V C
541/181 571/191
GGC ATG GTT TGC ATT GGG CCC AAT GTG CTT ATG GTA CAT AAA AGG AGT CAC ACT GGT GAA
G M V C I G P N V L M V H K R S H T G E
601/201 631/211
CGC CCC TTC CAC TGT AAC CAG TGT GGA GCT TCT TTT ACT CAG AAG GGC AAC CTT CTG AGA
R P F H C N Q C G A S F T Q K G N L L R
661/221 691/231
CAC ATA AAG TTA CAC TCT GGA GAG AAG CCG TTC AAA TGT CCT TTC TGT AGT CAC GCC TGT
H I K L H S G E K P F K C P F C S H A C
721/241 751/251
AGA AGA AGG GAC GCC CTC ACA GGA TAC CTC AGG ACC CAT TCT GTG GGT AAA CCT CAC AAG
R R R D A L T G Y L R T H S V G K P H K
781/261 811/271
TGC AAC TAC TGT GGA CGA AGC TAC AAG CAG CGC AGT TCA CTG GAG GAG CAC AAG GAA CGC
C N Y C G R S Y K Q R S S L E E H K E R
841/281 871/291
TGC CAC AAC TAT CTC CAG AAT GTC AGC ATG GAG GCT GCT GGG CAG GTC ATG AGT CAC CAT
C H N Y L Q N V S M E A A G Q V M S H H
901/301 931/311
GTA CCT CCT ATG GAA GAT TGT AAG GAA CAA GAG CCT ATT ATG GAC AAC AAT ATT TCT CTG
V P P M E D C K E Q E P I M D N N I S L
961/321 991/331
GTG CCT TTT GAG AGA CCT GCT GTC ATA GAG AAG CTC ACY GGG AAT ATG GGA AAA CGT AAA
V P F E R P A V I E K L T G N M G K R K
1021/341 1051/351
AGC TCC ACT CCA CAA AAG TTT GTG GGG GAA AAG CTC ATG CGA TTC AGC TAC CCA GAT ATT
S S T P Q K F V G E K L M R F S Y P D I
1081/361 1111/371
CAC TTT GAT ATG AAC TTA ACA TAT GAG AAG GAG GCT GAG CTG ATG CAG TCT CAT ATG ATG
H F D M N L T Y E K E A E L M Q S H M M
1141/381 1171/391
GAC CAA GCC ATC AAC AAT GCA ATC ACC TAC CTT GGA GCT GAG GCC CTT CAC CCT CTG ATG
D Q A I N N A I T Y L G A E A L H P L M
1201/401 1231/411
CAG CAC CCG CCA AGC ACA ATC GCT GAA GTG GCC CCA GTT ATA AGC TCA GCT TAT TCT CAG
Q H P P S T I A E V A P V I S S A Y S Q

FIG. 5A

1261/421 1291/431
GTC TAT CAT CCA AAT AGG ATA GAA AGA CCC ATT AGC AGG GAA ACT GCT GAT AGT CAT GAA
V Y H P N R I E R P I S R E T A D S H E
1321/441 1351/451
AAC AAC ATG GAT GCC CCC ATC TCT CTC ATC AGA CCA AAG AGT CGA CCC CAG GAA AGA GAG
N N M D G P I S L I R P K S R P Q E R E
1381/461 1411/471
GCC TCT CCC AGC AAT AGC TGC CTG GAT TCC ACT GAC TCA GAA AGC AGC CAT GAT GAC CAC
A S P S N S C L D S T D S E S S H D D H
1441/481 1471/491
CAG TCC TAC CAA GGA CAC CCT GCC TTA AAT CCC AAG AGG AAA CAA AGC CCA GCT TAC ATG
Q S Y Q G H P A L N P K R K Q S P A Y M
1501/501 1531/511
AAG GAG GAT GTC AAA GCT TTG GAT ACT ACC AAG GCT CCT AAG GCC TCT CTG AAG GAC ATC
K E D V K A L D T T K A P K G S L K D I
1561/521 1591/531
TAC AAG GTC TTC AAT GGG GAA GGA GAA CAG ATT AGG GCC TTC AAG TGT GAG CAC TGC CGA
Y K V F N G E G E Q I R A F K C E H C R
1621/541 1651/551
GTC CTT TTC CTA GAC CAT GTC ATG TAC ACC ATT CAC ATG GGT TGC CAT GCC TAC CGG GAC
V L F L D H V M Y T I H M G C H G Y R D
1681/561 1711/571
CCA CTG GAA TGT AAC ATC TGT GCC TAC AGA AGC CAG GAC CGT TAT GAG TTT TCA TCA CAC
P L E C N I C G Y R S Q D R Y E F S S H
1741/581 1771/591
ATT GTT CGA GGG GAG CAC ACA TTC CAC TAG GCC TTT TCA TTC CAA AGG GGA CCC TAT GAA
I V R G E H T F H * A F S F Q R G P Y E
1801/601 1831/611
GTA AAG ACT GCA CAT GAA GAA ATA CTG CAC TTA CAA TCC CAC CTT TCC TCA AAT GTT GTA
V K T A H E E I L H L Q S H L S S N V V
1861/621 1891/631
CCT TTT ATT TTT TTA ATA TAA TAC TCG TGA TAA TCT TAT TTT GTG GAG CAG TGT CAT TTG
P F I F L I * Y W * * S Y F V E Q C H L
1921/641
CTC TGC T
L C

FIG. 5B

1 ATGGAAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTC 50
190 ATGGAAACAGAGGCTATTGATGGCTATATAACGTGTGACAATGAGCTTTC 239
51 ACCCGAAGGGGAACACGCCAATATGCCATTGACCTCACCTCAAGCACGC 100
240 ACCCGAAAGGGAGCACTCCAATATGCAATTGACCTCACCTCAAGCACAC 289
101 CCAATGGACAGCAGCCTCGCCAAGTCACATGACAAGCACAATTCTGTA 150
290 CCAATGGACAGCATGCCACTCCAAGTCACATGACAAGCACAGATTCAAGTA 339
151 AAGCTGAAATGCAAGACTGATGAAGAGTGTGACAGGCAGCCCTGAGCCG 200
340 AAGCTAGAAATGCAAGACTGATGAAGAGTGTGACAGGAAACCCCTGAGCCG 389
201 TGAGGATGAGATCAGGGGCCACGATGAGGGAGCAGCCTAGAAGAACCCC 250
390 TGAAGATGAGATCAGGGCCATGATGAGGGTAGCAGCCTAGAAGAACCCC 439
251 TAATTGAGAGCAGCGAGGTGGCCGACAACAGGAAAGTCCAGGACCTCAA 300
440 TAATTGAGAGCAGCGAGGTGGCTGACAACAGGAAAGTCCAGGAGCTCAA 489
301 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 350
490 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 539
351 TGGCATGGTTGCATTGGGCCAATGTGCTTATGGTACATAAAAGGAGTC 400
540 TGGCATGGTTGCATTGGGCCAATGTGCTTATGGTACATAAAAGGAGTC 589
401 ACACGGTGAGCGGCCCTTCCACTGTAACCAGTGGAGCTTCTTTACC 450
590 ACACGGTGAGCGGCCCTTCCACTGTAACCAGTGGAGCTTCTTTACT 639
451 CAGAAGGGCAACCTCTGAGACACATAAAGTTACACTCTGGAGAGAACCC 500
640 CAGAAGGGCAACCTCTGAGACACATAAAGTTACACTCTGGAGAGAACCC 689
501 CTTCAAATGTCCTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCA 550
690 GTTCAAATGTCCTTCTGTAGTCACGCCGTAGAAGAAGGGACGCCCTCA 739
551 CAGGACACCTCAGGACCCATTCTGTGGTAAACCTCACAAGTGTAACTAC 600
740 CAGGATAACCTCAGGACCCATTCTGTGGTAAACCTCACAAGTGTAACTAC 789
601 TGTGGCCGAAGCTACAAGCAGCGCACGTCACTGGAGGAACACAAGGAACG 650
790 TGTGGACGAAGCTACAAGCAGCGCAGTTACTGGAGGAACACAAGGAACG 839
651 CTGTCACAACATCTCCAGAATGTCAGCATGGAGGTGCCCCAGGTCA 700
840 CTGCCACAACATCTCCAGAATGTCAGCATGGAGGTGCTGGCAGGTCA 889
701 TGAGTCACCATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATC 750
890 TGAGTCACCATGTACCTCCTATGGAAGATTGTAAGGAACAAGAGCCTATT 939
751 ATGGACACAAATATTCTCTGGTGCCTTGTGAGAGACCTGCTGTCAAGA 800

FIG. 6A

940 ATGGACAAACAATATTCTCTGGTGCCTTGAGAGACCTGCTGTCACTAGA 989
801 GAAGCTCACGGCAAATATGGGAAAGCGCAAAGCTCCACTCCTCAGAAGT 850
990 GAAGCTCACGGGAATATGGGAAAACGTAAAAGCTCCACTCCACAAAAAGT 1039
851 TTGTGGGGAAAAGCTTATGCATTGAGCTACCCAGATATTCACTTTGAT 900
1040 TTGTGGGGAAAAGCTCATGCATTGAGCTACCCAGATATTCACTTTGAT 1089
901 ATGAACCTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 950
1090 ATGAACCTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 1139
951 GGACCAAGCCATCAACAATGCAATCACCTACCTGGAGCTGAGGCCCTTC 1000
1140 GGACCAAGCCATCAACAATGCAATCACCTACCTGGAGCTGAGGCCCTTC 1189
1001 ACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTT 1050
1190 ACCCTCTGATGCAGCACCGCCAAGCACAATCGCTGAAGTGGCCCCAGTT 1239
1051 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACC 1100
1240 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAATAGGATAGAAAGACC 1289
1101 CATTAGCAGGGAAACATCTGATAAGTCACGAAAACAACATGGATGGCCCCA 1150
1290 CATTAGCAGGGAAACTGCTGATAAGTCATGAAAACAACATGGATGGCCCCA 1339
1151 TCTCTCTCATCAGACCAAAGAGTCGACCCAGGAAAGAGAGGCCCTCGCCC 1200
1340 TCTCTCTCATCAGACCAAAGAGTCGACCCAGGAAAGAGAGGCCCTCTCCC 1389
1201 AGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCG 1250
1390 AGCAATAGCTGCCTGGATTCCACTGACTCAGAAAGCAGCCATGATGACCA 1439
1251 CCAGTCCTACCAAGGAAACCCCTGCCTTAATCCAAGAGGAAACAAAGCC 1300
1440 CCAGTCCTACCAAGGACACCCCTGCCTTAATCCAAGAGGAAACAAAGCC 1489
1301 CAGCTTACATGAAGGAGGATGTCAAGGCTTGGATGCTACCAAGGCCCTC 1350
1490 CAGCTTACATGAAGGAGGATGTCAAAGCTTGGATACTACCAAGGCTCCT 1539
1351 AAGGGCTCTCTGAAGGACATCTATAAGGTTTCAATGGAGAAGGAGAAC 1400
1540 AAGGGCTCTCTGAAGGACATCTACAAGGTCTCAATGGGAAGGAGAAC 1589
1401 GATAAGGGCTTCAAGTGTGAGCACTGCCAGTCCTTTCTAGACCATG 1450
1590 GATTAGGGCTTCAAGTGTGAGCACTGCCAGTCCTTTCTAGACCATG 1639
1451 TCATGTACACCATTCACATGGGTGCCATGGCTACCGGGACCCACTGGAA 1500
1640 TCATGTACACCATTCACATGGGTGCCATGGCTACCGGGACCCACTGGAA 1689
1501 TGCAACATCTGTGGCTACAGAACGCCAGGACCGTACGAATTTCATCACA 1550
1690 TGTAACATCTGTGGCTACAGAACGCCAGGACCGTTATGAGTTTCATCACA 1739
1551 CATTGTTGGGGGCAGCACACATTCCACTAGGCAGTGCATTCAAGG 1598
1740 CATTGTTGAGGGAGCACACATTCCACTAGGCCTTTCATTCAAAG 1787

1 METEAIDGYITCDNELSPEREHSNMAIDLTSSTPNGQHASPSHMTSTDV 50
1 METEAIDGYITCDNELSPEREHSNMAIDLTSSTPNGQHASPSHMTSTDV 50
51 KLEMQSDEECDRKPLSREDEIRGHDEGSSLEEPLIESSEVADNREVQELQ 100
51 KLEMQSDEECDRKPLSREDEIRGHDEGSSLEEPLIESSEVADNREVQELQ 100
101 GEGGIRLPNGKLKCDVCGMVICGPNVLMVHKRSHTGERPFHCNCQCGASFT 150
101 GEGGIRLPNGKLKCDVCGMVICGPNVLMVHKRSHTGERPFHCNCQCGASFT 150
151 QKGNLLRHILHSGEKPKCPFCSHACRRRDALTGYLRTHSGVKPHKCNY 200
151 QKGNLLRHILHSGEKPKCPFCSHACRRRDALTGYLRTHSGVKPHKCNY 200
201 CGRSYKQRSSLEEHKERCHNYLQNVSMEEAGQVMSSHVPMPMEDCKEQEPI 250
201 CGRSYKQRSSLEEHKERCHNYLQNVSMEEAGQVMSSHVPMPMEDCKEQEPI 250
251 MDNNISLVPFERPAVIEKLTGNGKRSSTPQKFVGEKLMRFSYVDIHF 300
251 MDNNISLVPFERPAVIEKLTGNGKRSSTPQKFVGEKLMRFSYVDIHF 300
301 MNLTYEKEAELMQSHMDQAINNAITYLGAEALHPLMQHPPSTIAEVAPV 350
301 MNLTYEKEAELMQSHMDQAINNAITYLGAEALHPLMQHPPSTIAEVAPV 350
351 ISSAYSQVYHPNRIERPISRETADSHENNMDGPISLIRPKSRPQEAREASP 400
351 ISSAYSQVYHPNRIERPISRETADSHENNMDGPISLIRPKSRPQEAREASP 400
401 SNSCLDSTDSESSHDDHQSYQGHPALNPKRQSPAYMKEDVKALDTTKAP 450
401 SNSCLDSTDSESSHDDHQSYQGHPALNPKRQSPAYMKEDVKALDTTKAP 450
451 KGSLKDIYKVFNQGEQIRAFKCEHCRVLFLDHVMYTIHMGCHGYRDPLE 500
451 KGSLKDIYKVFNQGEQIRAFKCEHCRVLFLDHVMYTIHMGCHGYRDPLE 500
501 CNICGYRSQDRYEFSSHIVRGEHTFH 526
501 CNICGYRSQDRYEFSSHIVRGEHTFH 526

FIG. 7